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TECHNICAL DRAWING

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51502

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/623,304A

DATE: 05/06/2002

TIME: 14:23:25

Input Set : A:\185124-1.app

Output Set: N:\CRF3\05062002\I623304A.raw

```

3 <110> APPLICANT: Silvia, Christopher
4     Yu, Weifeng
5     ICAgen, Inc.
7 <120> TITLE OF INVENTION: Identification and Expression of Human Kir5.1
9 <130> FILE REFERENCE: 018512-000410US
11 <140> CURRENT APPLICATION NUMBER: US 09/623,304A
12 <141> CURRENT FILING DATE: 2001-02-21
14 <150> PRIOR APPLICATION NUMBER: US 60/076,612
15 <151> PRIOR FILING DATE: 1998-03-03
17 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/04549
18 <151> PRIOR FILING DATE: 1999-03-02
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 383
26 <212> TYPE: PRT
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <223> OTHER INFORMATION: human Kir5.1 alpha subunit monomer of inward
31     rectifier potassium channel
33 <220> FEATURE:
34 <221> NAME/KEY: PEPTIDE
35 <222> LOCATION: (351)..(383)
36 <223> OTHER INFORMATION: tail region
38 <220> FEATURE:
39 <221> NAME/KEY: MOD_RES
40 <222> LOCATION: (303)
41 <223> OTHER INFORMATION: Xaa = Lys or Glu
43 <400> SEQUENCE: 1
44 Met Ser Tyr Tyr Gly Ser Ser Tyr His Ile Ile Asn Ala Asp Ala Lys
45 1         5         10         15
46 Tyr Pro Gly Tyr Pro Pro Glu His Ile Ile Ala Glu Lys Arg Arg Ala
47         20         25         30
48 Arg Arg Arg Leu Leu His Lys Asp Gly Ser Cys Asn Val Tyr Phe Lys
49         35         40         45
50 His Ile Phe Gly Glu Trp Gly Ser Tyr Val Val Asp Ile Phe Thr Thr
51         50         55         60
52 Leu Val Asp Thr Lys Trp Arg His Met Phe Val Ile Phe Ser Leu Ser
53 65         70         75         80
54 Tyr Ile Leu Ser Trp Leu Ile Phe Gly Ser Val Phe Trp Leu Ile Ala
55         85         90         95
56 Phe His His Gly Asp Leu Leu Asn Asp Pro Asp Ile Thr Pro Cys Val
57         100        105        110

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58 Asp Asn Val His Ser Phe Thr Gly Ala Phe Leu Phe Ser Leu Glu Thr  
 59 115 120 125  
 60 Gln Thr Thr Ile Gly Tyr Gly Tyr Arg Cys Val Thr Glu Glu Cys Ser  
 61 130 135 140  
 62 Val Ala Val Leu Met Val Ile Leu Gln Ser Ile Leu Ser Cys Ile Ile  
 63 145 150 155 160  
 64 Asn Thr Phe Ile Ile Gly Ala Ala Leu Ala Lys Met Ala Thr Ala Arg  
 65 165 170 175  
 66 Lys Arg Ala Gln Thr Ile Arg Phe Ser Tyr Phe Ala Leu Ile Gly Met  
 67 180 185 190  
 68 Arg Asp Gly Lys Leu Cys Leu Met Trp Arg Ile Gly Asp Phe Arg Pro  
 69 195 200 205  
 70 Asn His Val Val Glu Gly Thr Val Arg Ala Gln Leu Leu Arg Tyr Thr  
 71 210 215 220  
 72 Glu Asp Ser Glu Gly Arg Met Thr Met Ala Phe Lys Asp Leu Lys Leu  
 73 225 230 235 240  
 74 Val Asn Asp Gln Ile Ile Leu Val Thr Pro Val Thr Ile Val His Glu  
 75 245 250 255  
 76 Ile Asp His Glu Ser Pro Leu Tyr Ala Leu Asp Arg Lys Ala Val Ala  
 77 260 265 270  
 78 Lys Asp Asn Phe Glu Ile Leu Val Thr Phe Ile Tyr Thr Gly Asp Ser  
 79 275 280 285  
 W--> 80 Thr Gly Thr Ser His Gln Ser Arg Ser Ser Tyr Val Pro Arg Xaa Ile  
 81 290 295 300  
 82 Leu Trp Gly His Arg Phe Asn Asp Val Leu Glu Val Lys Arg Lys Tyr  
 83 305 310 315 320  
 84 Tyr Lys Val Asn Cys Leu Gln Phe Glu Gly Ser Val Glu Val Tyr Ala  
 85 325 330 335  
 86 Pro Phe Cys Ser Ala Lys Gln Leu Asp Trp Lys Asp Gln Gln Leu His  
 87 340 345 350  
 88 Ile Glu Lys Ala Pro Pro Val Arg Glu Ser Cys Thr Ser Asp Thr Lys  
 89 355 360 365  
 90 Ala Arg Arg Arg Ser Phe Ser Ala Val Ala Ile Val Ser Ser Trp  
 91 370 375 380  
 94 <210> SEQ ID NO: 2  
 95 <211> LENGTH: 1509  
 96 <212> TYPE: DNA  
 97 <213> ORGANISM: Homo sapiens  
 99 <220> FEATURE:  
 100 <223> OTHER INFORMATION: human Kir5.1 alpha subunit monomer of inward  
 101 rectifier potassium channel  
 103 <220> FEATURE:  
 104 <221> NAME/KEY: CDS  
 105 <222> LOCATION: (46)..(1197)  
 106 <223> OTHER INFORMATION: human Kir5.1 alpha subunit  
 108 <220> FEATURE:  
 109 <221> NAME/KEY: unsure  
 110 <222> LOCATION: (1279)  
 111 <223> OTHER INFORMATION: n = a, g, c or t

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113 &lt;400&gt; SEQUENCE: 2

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114 ttactactac aaaactcacc tggatcccta agggcacagc aaagaatgag ctattacggc 60
115 agcagctatc atattatcaa tgcggacgca aaataccagc gctacccgcc agagcacatt 120
116 atagctgaga agagaagagc aagaagacga ttacttcaca aagatggcag ctgtaatgtc 180
117 tacttcaagc acatTTTTtg agaatgggga agctatgtgg ttgacatctt caccactctt 240
118 gtggacacca agtggcgcca tatgtttgtg atattttctt tatcttata tctctcgtgg 300
119 ttgatatttg gctctgtctt ttggctcata gcctttcacc atggcgatct attaaatgat 360
120 ccagacatca caccttgtgt tgacaacgct cattctttca caggggcctt tttgttctcc 420
121 ctagagaccc aaaccacatc aggatattgg tatcgtctgt ttactgaaga atgttctgtg 480
122 gccgtgctca tggtgatcct ccagtccatc ttaagttgca tcataaatac ctttatcatt 540
123 ggagctgcct tggccaaaat ggcaactgct cgaaagagag cccaaaccat tcgtttcagc 600
124 tactttgcac ttataggtat gagagatggg aagctttgcc tcatgtggcg cattggtgat 660
125 tttcggccaa accacgtggg agaaggaaca gtagagccc aacttctccg ctatacagaa 720
126 gacagtgaag ggaggatgac gatggcattt aaagacctca aattagtcaa cgaccaaata 780
127 atcctggtca ccccggtaac tattgtccat gaaattgacc atgagagccc tctgtatgcc 840
128 cttgaccgca aagcagtagc caaagataac tttgagattt tggtagacatt tatctatact 900
129 ggtgattcca ctggaacatc tcaccaatct agaagctcct atgttccccg araaattctc 960
130 tggggccata ggtttaatga tgtcttgaa gttaagagga agtattacaa agtgaactgc 1020
131 ttacagtttg aagggaagtgt ggaagtatat gccccctttt gcagtgccaa gcaattggac 1080
132 tggaaagacc agcagctcca catagaaaaa gcaccaccag ttcgagaatc ctgcacgtcg 1140
133 gacaccaagg cgagacgaag gtcatttagt gcagttgcc a ttgtcagcag ctggtgaaaa 1200
134 ccctgaggag accaccactt tcgccacaca tgaatatagg gaaacacctt atcagaaaagc 1260
W--> 135 tctccctgac tttaaacang aatcctctgt wgaatcccaa atgttagtcc taaaattgca 1320
136 attatgaggg ctaccactga atcattttat ctttcagcca atcaagtcgt tgtaaactgt 1380
137 gcttttttga aagtgttatg gctatgtttt atgatgatgc tgggtaagta gagtaagtta 1440
138 aacttggtaa agataatct aaaaattcca tagttctcag ttattaaaat ttttcttgtt 1500
139 ccggaattc 1509

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141 &lt;210&gt; SEQ ID NO: 3

142 &lt;211&gt; LENGTH: 24

143 &lt;212&gt; TYPE: DNA

144 &lt;213&gt; ORGANISM: Artificial Sequence

146 &lt;220&gt; FEATURE:

147 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:primer

149 &lt;400&gt; SEQUENCE: 3

150 cctaagggca cagcaaagaa tgag 24

152 &lt;210&gt; SEQ ID NO: 4

153 &lt;211&gt; LENGTH: 20

154 &lt;212&gt; TYPE: DNA

155 &lt;213&gt; ORGANISM: Artificial Sequence

157 &lt;220&gt; FEATURE:

158 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence:primer

160 &lt;400&gt; SEQUENCE: 4

161 gtgtggcgaa agtggtggtc 20

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 05/06/2002  
PATENT APPLICATION: US/09/623,304A      TIME: 14:23:26

Input Set : A:\185124-1.app  
Output Set: N:\CRF3\05062002\I623304A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 303

Seq#:2; N Pos. 1279

**VERIFICATION SUMMARY**

DATE: 05/06/2002

PATENT APPLICATION: US/09/623,304A

TIME: 14:23:26

Input Set : A:\185124-1.app

Output Set: N:\CRF3\05062002\I623304A.raw

L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:288

L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1260